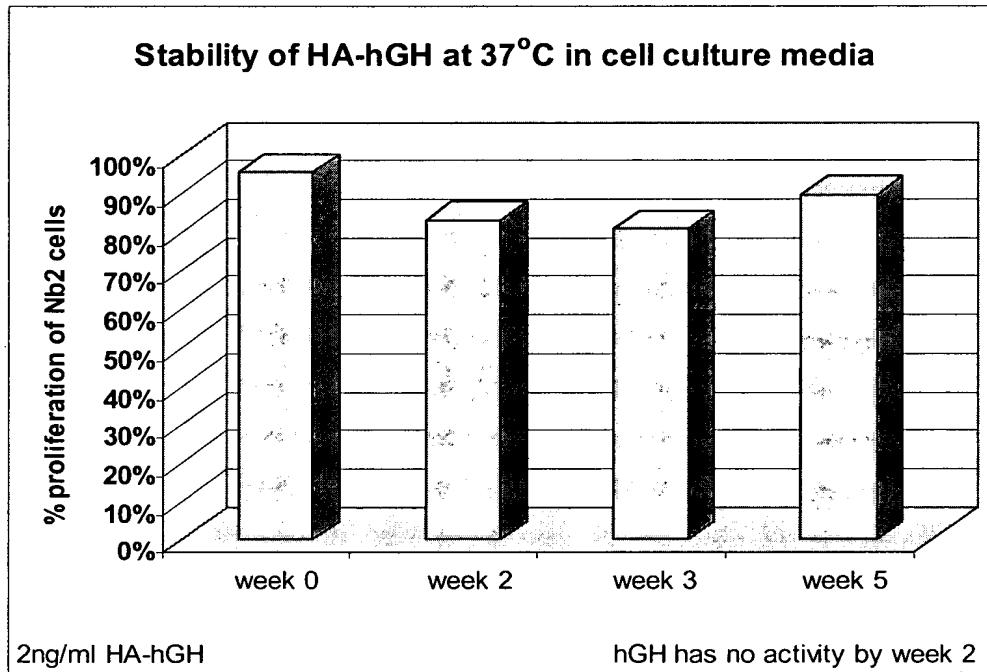
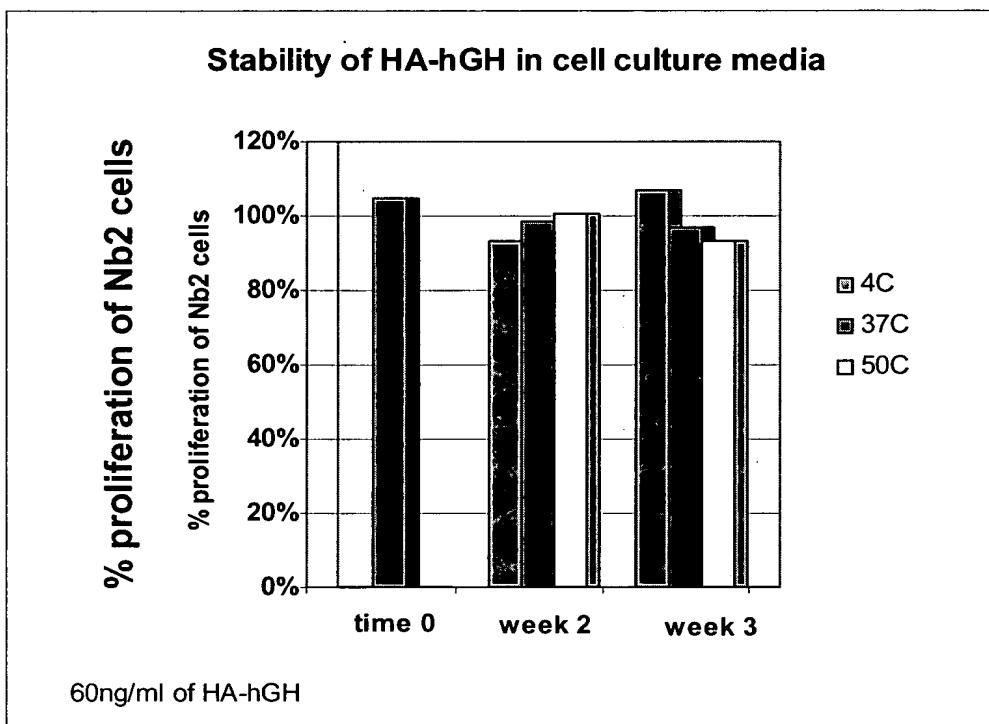


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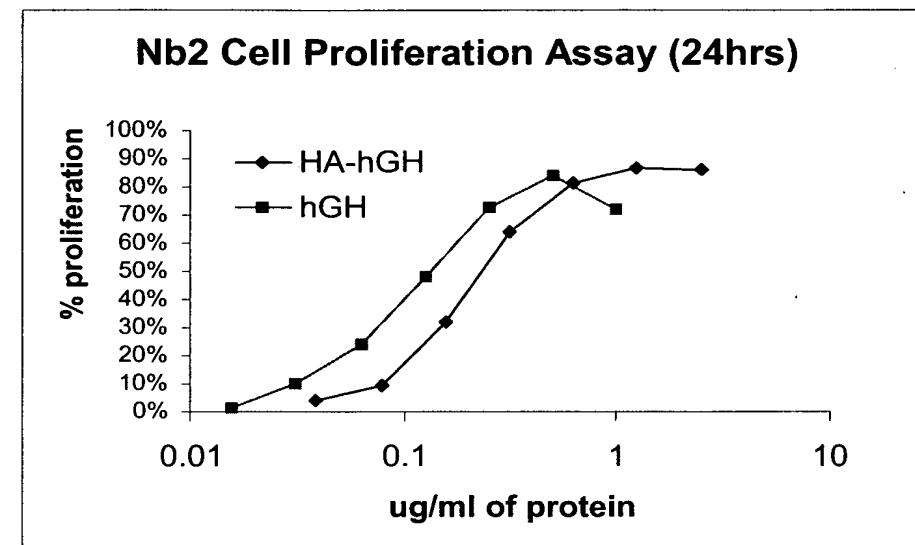


**Figure 1**

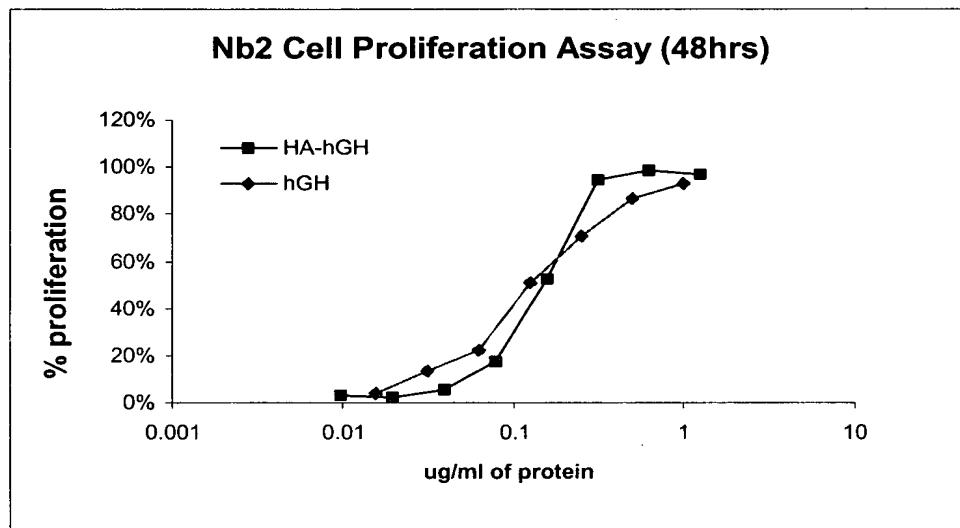


**Figure 2**

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**Figure 3A**



**Figure 3B**

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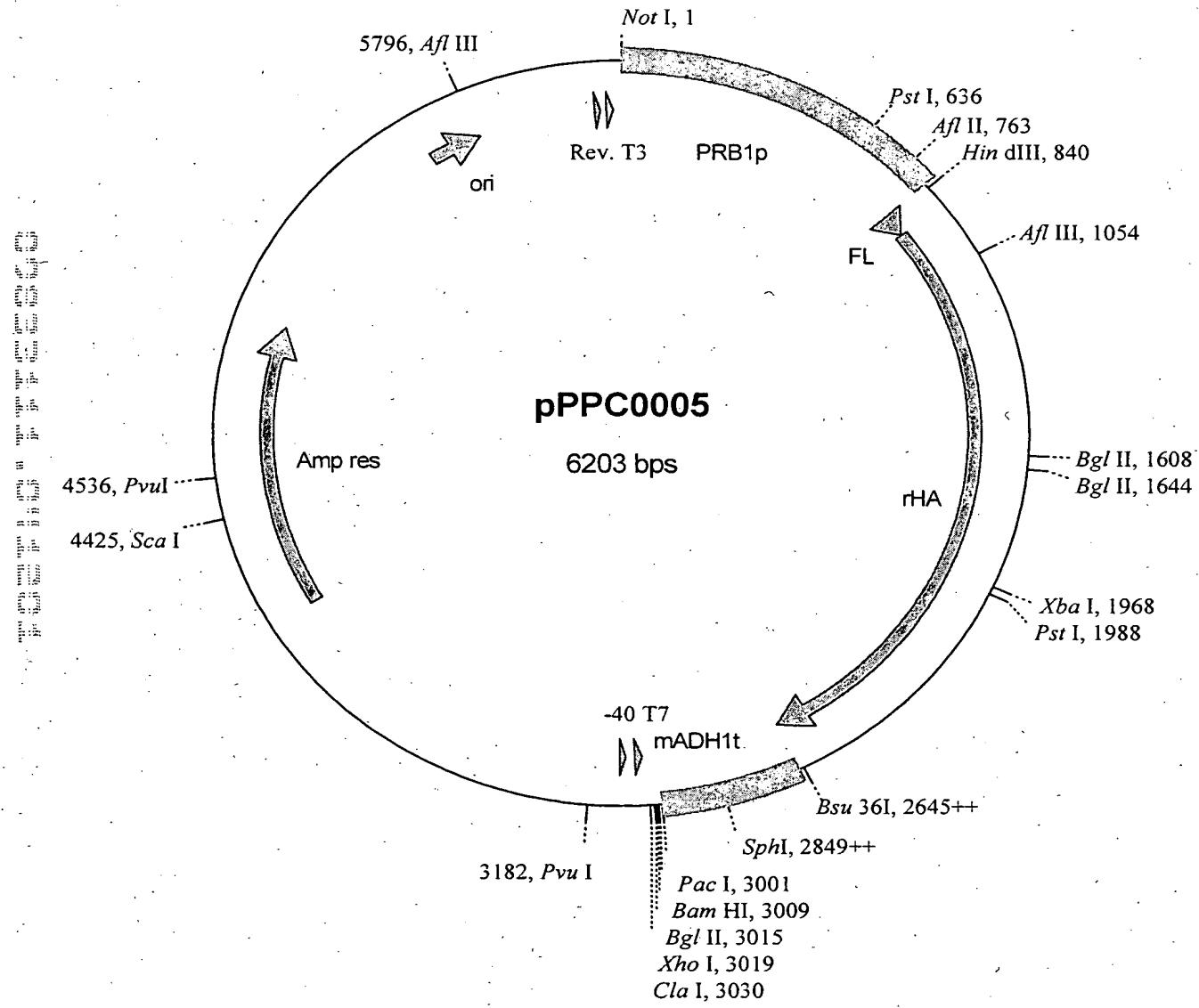
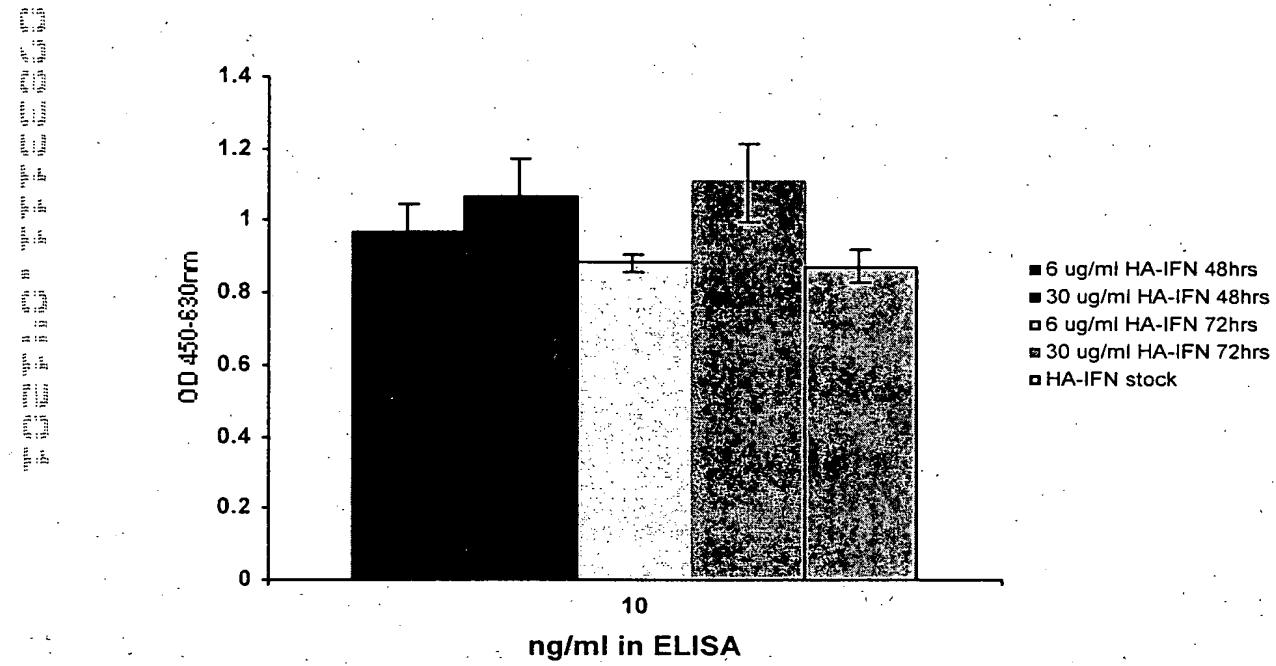


Figure 4

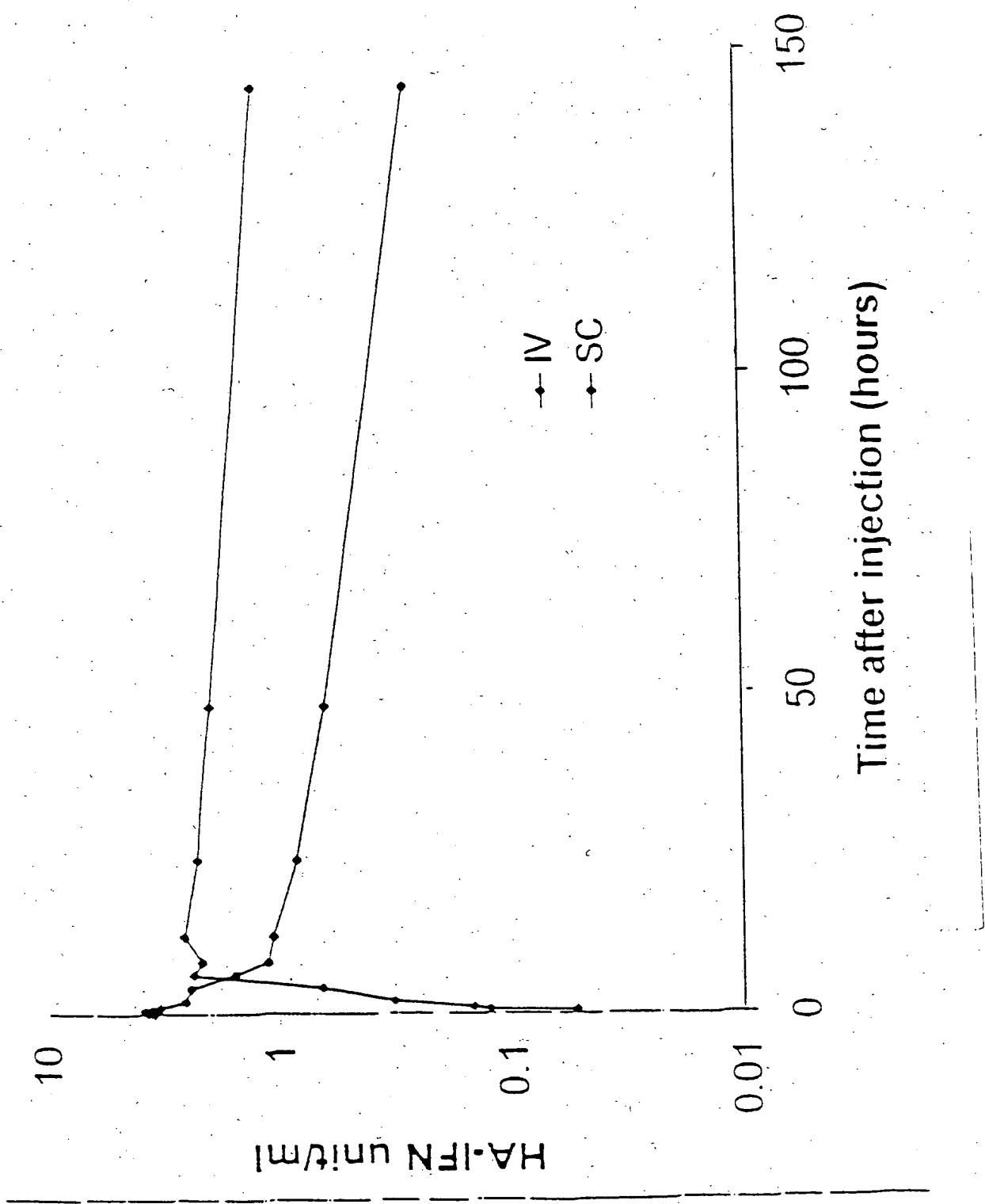
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**Figure 5**

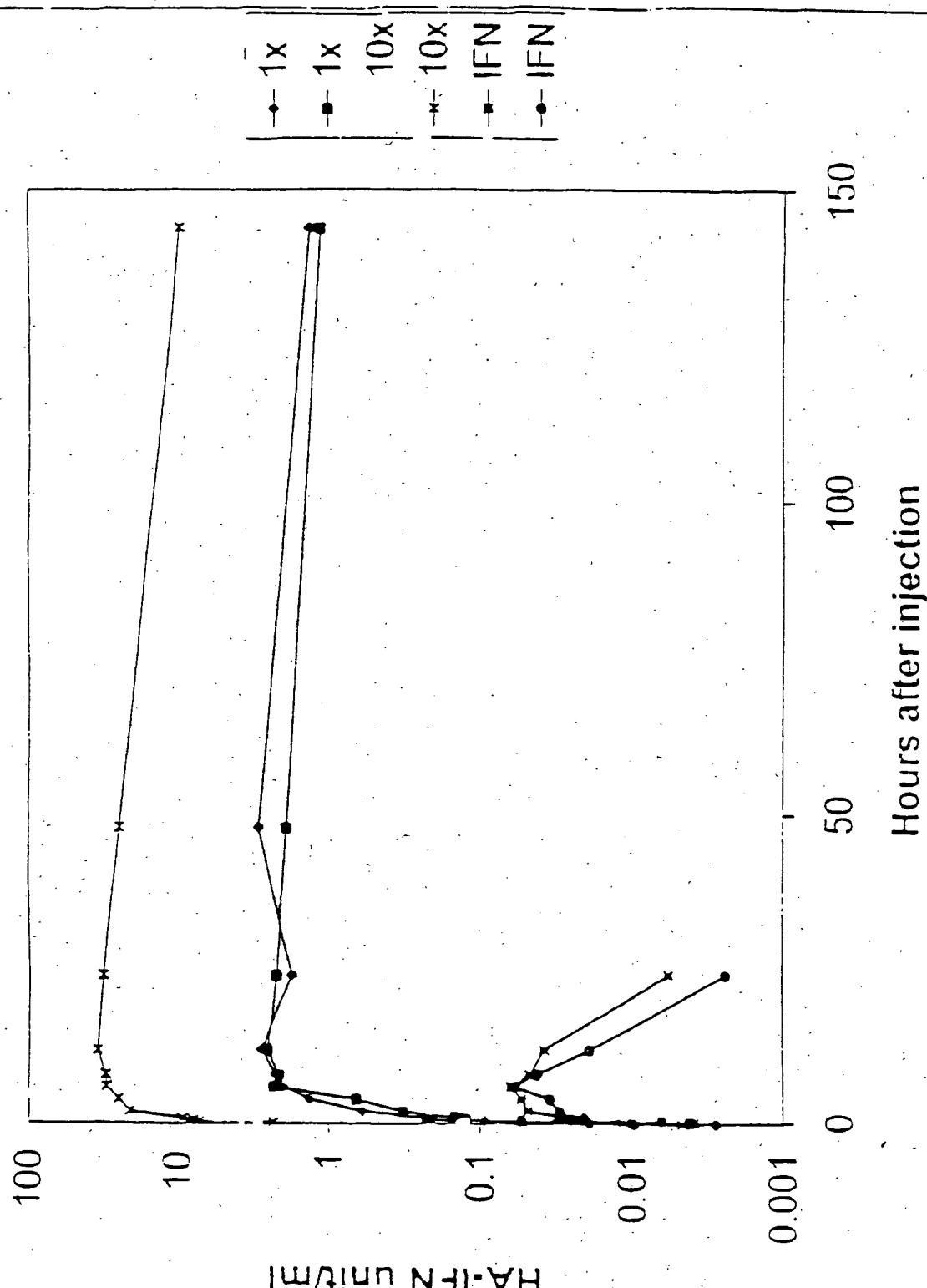
SCANNED, # 12

Figure 6

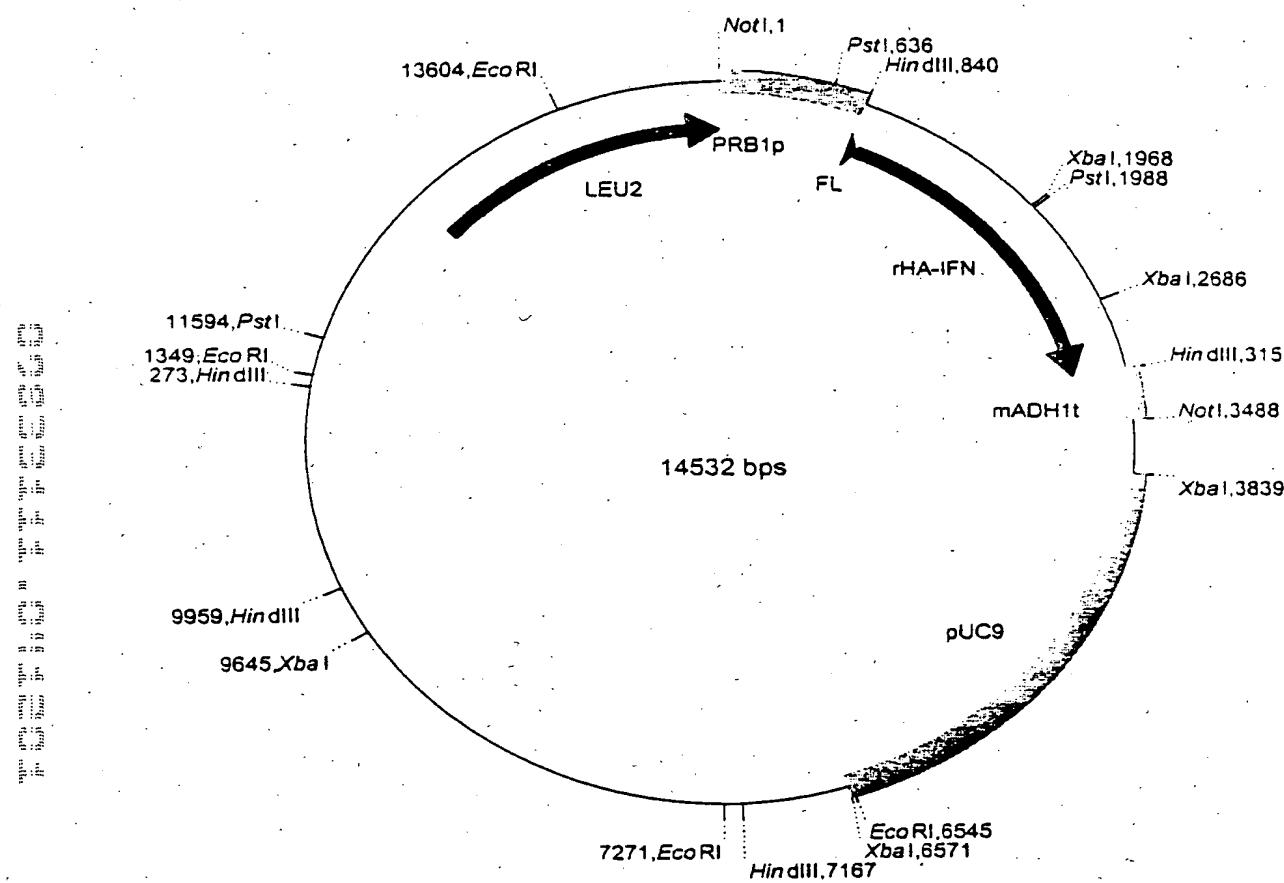


SCANNED, # 12

Figure 7



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**Figure 8.** The HA-IFN $\alpha$  expression cassette in pSAC35. The expression cassette comprises

PRB1 promoter, from *S. cerevisiae*.

Fusion leader, first 19 amino acids of the HA leader followed by the last 6 amino acids of the MF $\alpha$ -1 leader.

HA-IFN $\alpha$  coding sequence with a double stop codon (TAATAA)

ADH1 terminator, from *S. cerevisiae*. Modified to remove all the coding sequence normally present in the Hind III/BamHI fragment generally used.

**Figure 8**

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## Localisation of ‘Loops’ based on the HA Crystal Structure which could be used for Mutation/Insertion

1 DAHKSEVAHR FKDLGEENFK ALVIAFAQY LQQCPFEDHV KLVNEVTEFA  
HHHHH HHH HHH HHHHHHHHHHH HHHHH HHHHHHHHHHH

I II III

51 KTCVADESAE NCDKSLHTLF GDKLCTVATL RETYGEMADC CAKOEPERNE  
HHHHH HHHHH HHHHH HHH H HHHHH

101 CFLQHKDDNP NLPRLVLRPEV DVMCTAFHDN EETFLKKYLY EIARRHPYFY  
HHHH H HHHHHHHHH HHHHHHHHH HHHHH

IV

151 APELLFFAKR YKAATTECCO AADKAACLLP KLDELRLDEKG ASSAKQLKC  
HHHHHHHHHH HHHHHHHHH HHHHH HHHEHHHHHH HHHHHHHHHHH

V

201 ASLQKFGERA FKAWAVARLS QRFPKAFAE VSCLVTDLTK VHTECCGDL  
HHHHH HH HHHHHHHHHHH HH HHH HHHHHHHHHHH HHHHH HH

VI VII

251 LECADDRADL AKYICENODS ISSKLKECCE KPLLEKSHCI AEVENDEMPA  
HHHHHHHHHH HHHHH HHHHH HHHHHHH H

301 DLPSLAADFV ESKDVCKNYA EAKDVFLGMF LYEYARRHPD YSVVLLRLA  
HHHH HHHHH HHHHHHH HHHHH HHHHHHHHHHH

VIII

351 KTYETTLEKC CAAADPHECY AKVFDEFKPL VEEPQNLIKQ NCelféQLGE  
HHHHHHHHHH HH H HHHHH HHHHHHHHHHH HHHHHHH

IX

401 YKFQNALLVR YTAKVVPQVST PTLVEVSRNL GKVGSKCCKH PEAKRMPCAE  
HHHHHHHHHH HHHH H HHHHHHHHHHH HHH HHHHHHHHH

X XI

451 DYLSVVLNQL CVLHEKTPVS DRVTKCCTES LVNRPPCFSA LEVDETYVPK  
HHHHHHHHHH HHHHH HHHHHHHHH HHHHHHHHH

501 EFNAETFTFH ADICTLSEKE RQIKKQTALV ELVKHKPKAT KEQLKAVMDD  
HHH HHH HHHHHMMEEHHH HHH HHHHHHHHH

XII

551 FAAFVEKCCK ADDKETCFAE EGKKLVAASQ AALGL  
HHHHHHHH HHHHH HHHHHHHHHHH HH

<b>Loop</b>		<b>Loop</b>	
I	Val54-Asn61	VII	Glu280-His288
II	Thr76-Asp89	VIII	Ala362-Glu368
III	Ala92-Glu100	IX	Lys439-Pro447
IV	Gln170-Ala176	X	Val462-Lys475
V	His247-Glu252	XI	Thr478-Pro486
VI	Glu266-Glu277	XII	Lys560-Thr566

**Figure 9**

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## Examples of Modifications to Loop IV

#### a. Randomisation of Loop IV:

IV  
151 APELLFFAKR YKAATTECCQ AADKAACLLP KLDELRLDEGK ASSAKQLKC  
HHHHHHHHHHH HHHHHHHHHH HHHHH HHHHHHHHHHHH HHHHHHHHHHH

IV  
151 APELLFFAKR YKAAFTECCX XXXXXXCLLP KLDDELRLDEGK ASSAKQRLKC  
HHHHHHHHHH HHHHHHHHHH HHHHH HHHHHHHHHHH HHHHHHHHHH

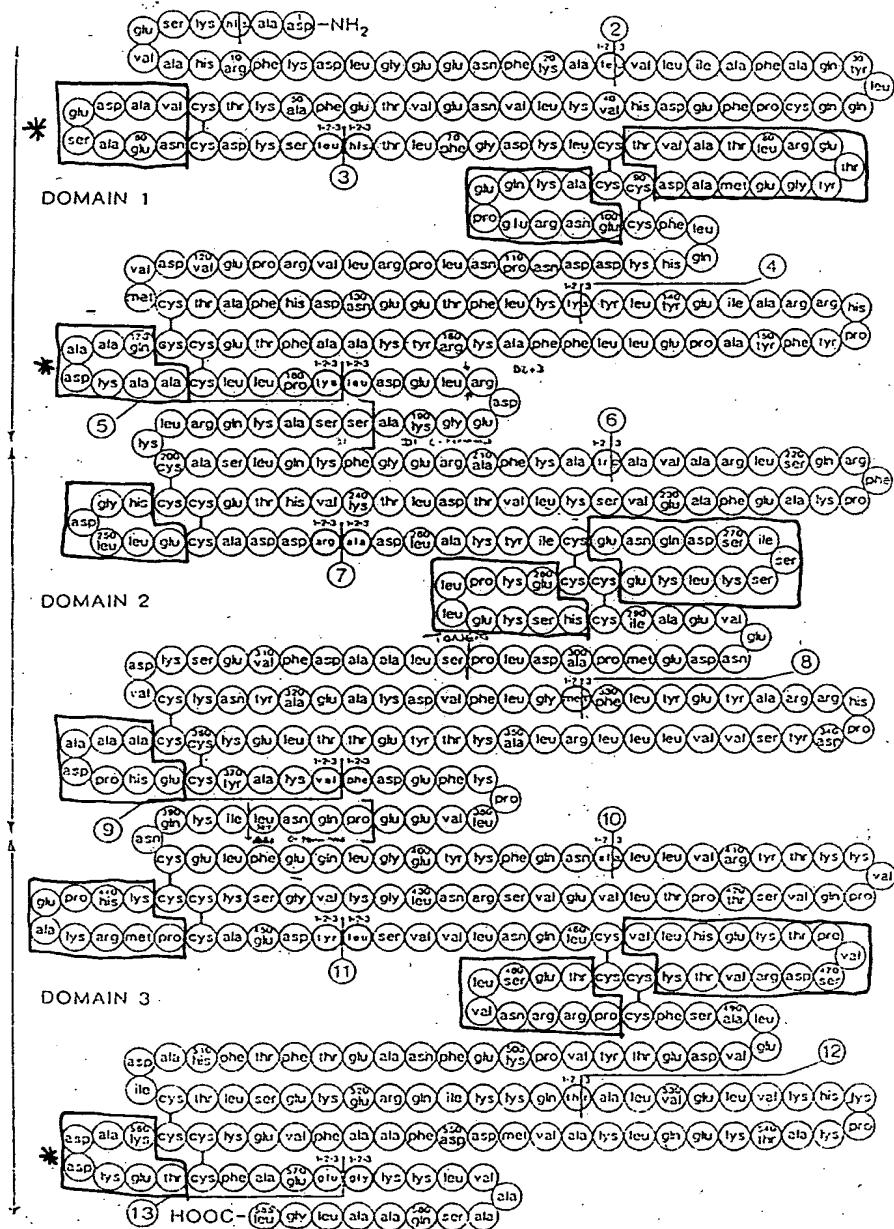
**X** represents the mutation of the natural amino acid to any other amino acid. One, more or all of the amino acids can be changed in this manner. This figure indicates all the residues have been changed.

**b. Insertion (or replacement) of Randomised sequence into Loop IV.**



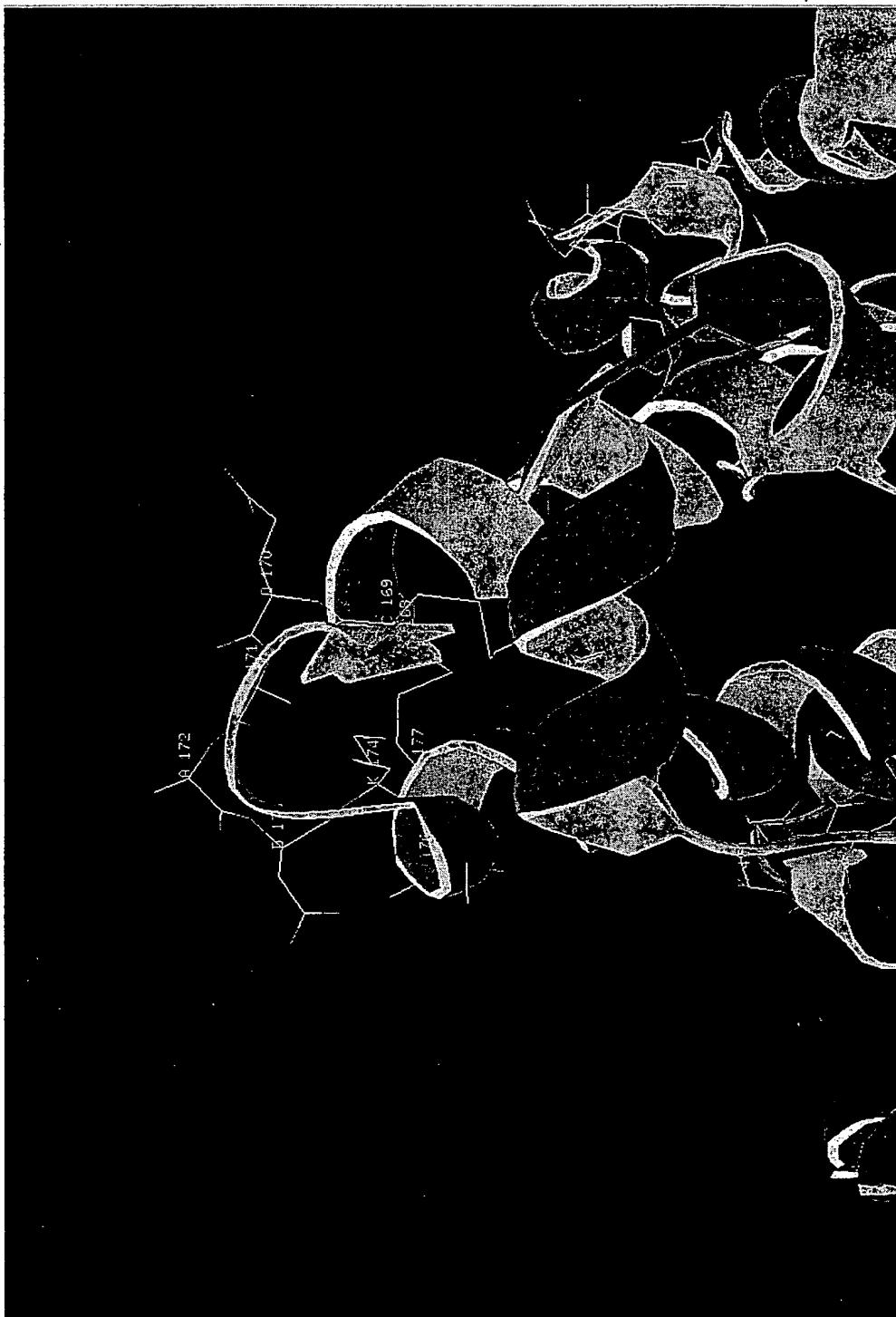
The insertion can be at any point on the loop and the length a length where  $n$  would typically be 6, 8, 12, 20 or 25.

**Figure 10**



**Figure 11**

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Disulfide bonds shown in yellow

Figure 12: Loop IV Gln170-Ala176

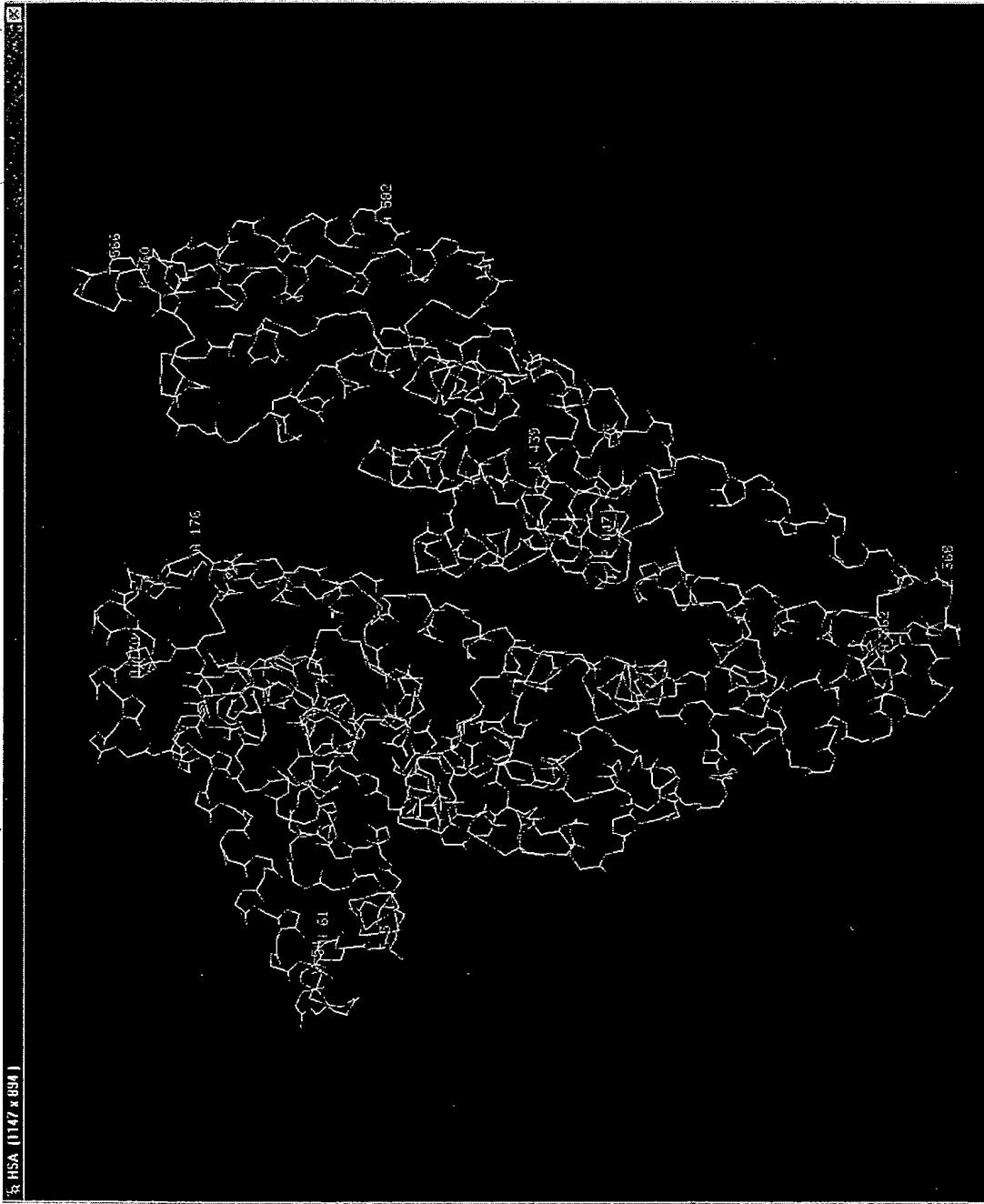


Figure 13: Tertiary Structure of HSA

ஏன் முதல் ஒரு நூலில் அதே போன்ற விவரம் கிடைக்கிறது.

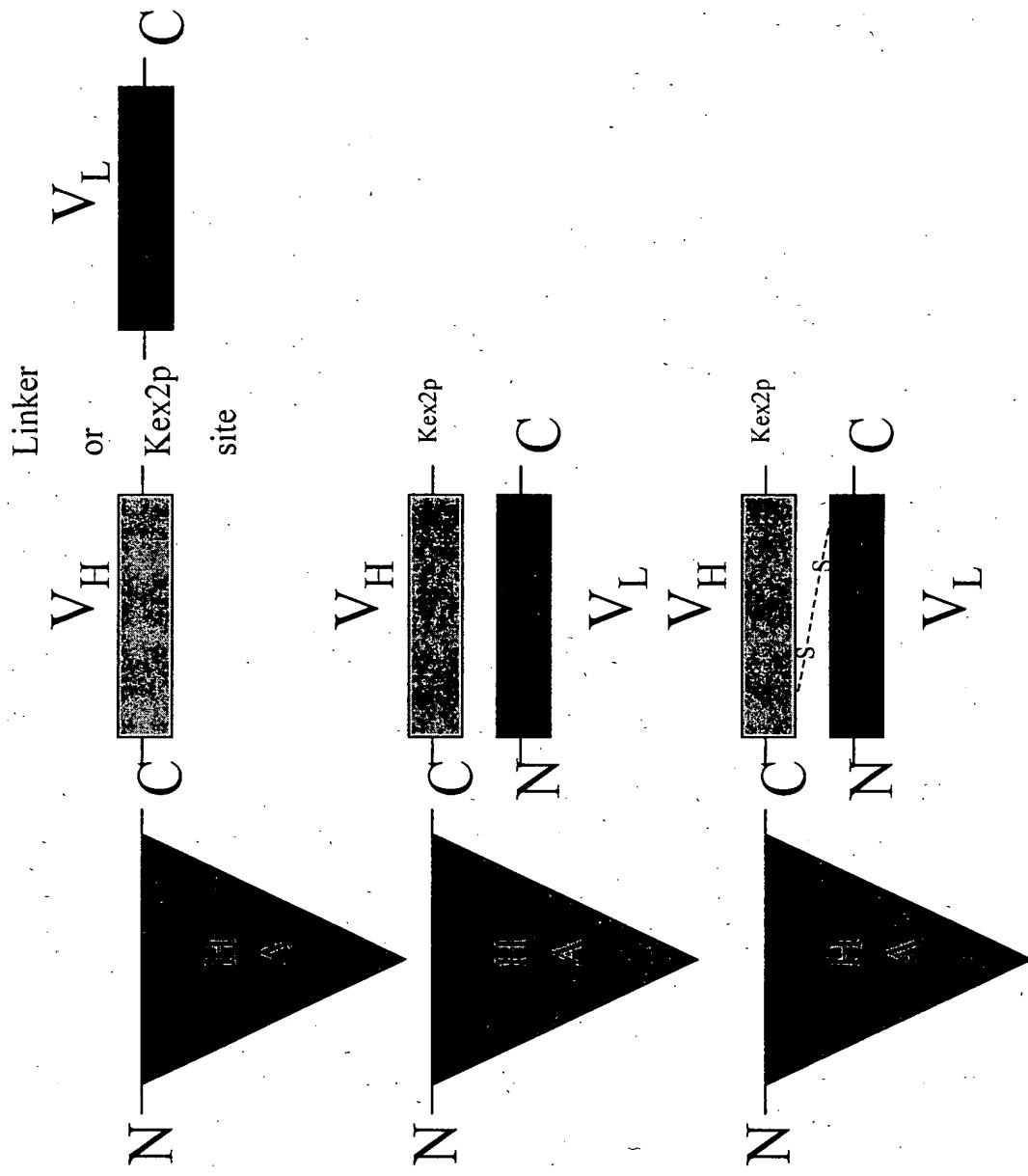


Figure 14: Schematic Diagram of Possible ScFv Fusions  
(Example is of a C-terminal fusion to HA)

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1 GAT GCA CAC AAG AGT GAG GTT GCT CAT CGG TTT AAA GAT TTG GGA GAA GAA AAT TTC AAA 60  
1 D A H K S E V A R F K D L G E E N F K 20

61 GCC TTG GTG TTG ATT GCC TTT GCT CAG TAT CTT CAG CAG TGT CCA TTT GAA GAT CAT GTA 120  
21 A L V L I A F A Q Y L Q C P F E D H V 40

121 AAA TTA GTG AAT GAA GTA ACT GAA TTT GCA AAA ACA TGT GTT GCT GAT GAG TCA GCT GAA 180  
41 K L V N E V T E F A K T C V A D E S A E 60

181 AAT TGT GAC AAA TCA CTT CAT ACC CTT TTT GGA GAC AAA TTA TGC ACA GTC GCA ACT CTT 240  
61 N C D K S L H T L F G D K L C T V A T L 80

241 CGT GAA ACC TAT GGT GAA ATG GCT GAC TGC TGT GCA AAA CAA GAA CCT GAG AGA AAT GAA 300  
81 R E T Y G E M A D C C A K Q E P E R N E 100

301 TGC TTC TTG CAA CAC AAA GAT GAC AAC CCA AAC CTC CCC CGA TTG GTG AGA CCA GAG GTT 360  
101 C F L Q H K D D N P N L P R L V R P E V 120

361 GAT GTG ATG TGC ACT GCT TTT CAT GAC AAT GAA GAG ACA TTT TTG AAA AAA TAC TTA TAT 420  
121 D V M C T A F H D N E E T F L K K Y L Y 140

421 GAA ATT GCC AGA AGA CAT CCT TAC TTT TAT GCC CCG GAA CTC CTT TTC TTT GCT AAA AGG 480  
141 E I A R R H P Y F V A P E L L F F A K R 160

Figure 15A

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481 TAT AAA GCT GCT TTT ACA GAA TGT TGC CAA GCT GCT GAT AAA GCT GCC TGC CTG TTT GCA 540  
161 Y K A A F T E C C Q A A D K A A C L L P 180

541 AAG CTC GAT GAA CTT CGG GAT GAA GGG AAG GCT TCG TCT GCC AAA CAG AGA CTC AAA TGT 600  
181 K L D E L R D E G K A S S A K Q R L K C 200

601 GCC AGT CTC CAA AAA TTT GGA GAA AGA GCT TTC AAA GCA TGG GCA GTG GCT CGC CTG AGC 660  
201 A S L Q K F G E R A F K A W V A R L S 220

661 CAG AGA TTT CCC AAA GCT GAG TTT GCA GAA GTT TCC AAG TTA GTG ACA GAT CTT ACC AAA 720  
221 Q R F P K A E F A E V S K L V T D L T K 240

721 GTC CAC ACG GAA TGC CAT GGA GAT CTG CTT GAA TGT GCT GAT GAC AGG GCG GAC CTT 780  
241 V H T E C C H G D L L E C A D D R A D L 260

781 GCC AAG TAT ATC TGT GAA AAT CAG GAT TCG ATC TCC AGT AAA CTG AAG GAA TGC TGT GAA 840  
261 A K Y I C E N Q D S I S S K L K E C C E 280

841 AAA CCT CTG TTG GAA AAA TCC CAC TGC ATT GCC GAA GTG GAA AAT GAT GAG ATG CCT GCT 900  
281 K P L L E K S H C I A E V E N D E M P A 300

901 GAC TTG CCT TCA TTA GCT GCT GAT TTT GTT GAA AGT AAG GAT GTT TGC AAA AAC TAT GCT 960  
301 D L P S L A D F V E S K D V C K N Y A 320

Figure 15B

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961 GAG GCA AAG GAT GTC TTC CTG GCC ATG TTT TTG TAT GAA TAT GCA AGA AGG CAT CCT GAT 1020  
321 E A K D V F L G M F L Y E Y A R R H P D 340

1021 TAC TCT GTC GTG CTG CTG AGA CTT GCC AAG ACA TAT GAA ACC ACT CTA GAG AAG TGC 1080  
341 Y S V L L R L A K T Y E T T L E K C 360

1081 TGT GCC GCT GCA GAT CCT CAT GAA TGC TAT GCC AAA GTG TTC GAT GAA TTT AAA CCT CTT 1140  
361 C A A D P H E C Y A K V F D E F K P L 380

1141 GTG GAA GAG CCT CAG AAT TTA ATC AAA CAA AAC TGT GAG CTT TTT GAG CAG CTT GGA GAG 1200  
381 V E E P Q N L I K Q N C E L F E Q L G E 400

1201 TAC AAA TTC CAG AAT GCG CTA TTA GTT CGT TAC ACC AAG AAA GTA CCC CAA GTG TCA ACT 1260  
401 Y K F Q N A L L V R Y T K V P Q V L S T 420

1261 CCA ACT CTT GTC TCA AGA AAC CTA GGA AAA GTG GGC AGC AAA TGT TGT AAA CAT 1320  
421 P T L V E V S R N L G K V G S K C C K H 440

1321 CCT GAA GCA AAA AGA ATG CCC TGT GCA GAA GAC TAT CTA TCC GTG GTC CTG AAC CAG TTA 1380  
441 P E A K R M P C A E D Y L S V V L N Q L 460

1381 TGT GTG TTG CAT GAG AAA ACG CCA GTA AGT GAC AGA GTC ACA AAA TGC TGC ACA GAG TCC 1440  
461 C V L H E K T P V S D R V T K C C T E S 480

Figure 15C

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1441 TTG GTG AAC AGG CGA CCA TGC TTT TCA GCT CTG GAA GTC GAT GAA ACA TAC GTT CCC AAA 1500  
481 L V N R R P C F S A L E V D E T Y V P K 500

1501 GAG TTT AAT GCT GAA ACA TTC ACC TTC CAT GCA GAT ATA TGC ACA CTT TCT GAG AAG GAG 1560  
501 E F N A E T F T P H A D I C T L S E K E 520

1561 AGA CAA ATC AAG AAA CAA ACT GCA CTT GTT GAG CTT GTG AAA CAC AAG CCC AAG GCA ACA 1620  
521 R Q I K K Q T A L V E L V K H K P K A T 540

1621 AAA GAG CAA CTG AAA GCT GTT ATG GAT GAT TTC GCA GCT TTT GTA GAG AAG TGC TGC AAG 1680  
541 K E Q L K A V M D D F A A F V E K C C K 560

1681 GCT GAC GAT AAG GAG ACC TGC TTT GCC GAG GAG GGT AAA AAA CTT GTT GCT GCA AGT CAA 1740  
561 A D D K E T C F A E E G K K L V A A S Q 580

1741 GCT GCC TTA GGC TTA TAA CAT CTA CAT TTA AAA GCA TCT CAG 1782  
581 A A L G L \* 585

**Figure 15D**